

### **Amendments to the Specification**

Please replace the paragraph beginning at page 8, line 8 with the following amended paragraph:

Wild type SPE-A toxin is encoded by a gene *speA* found on bacteriophage T12. The wild type SPE-A toxin has a molecular weight of 25,787 Daltons as calculated from the deduced amino acid sequence of the mature protein. A DNA sequence encoding a wild type SPE-A toxin and the predicted amino acid sequence for a wild type SPE-A toxin is shown in Figure 3. A DNA sequence encoding a wild type SPE-A toxin has been cloned in *E. coli* and *S. aureus*. Amino acid number designations in this application are made by reference to the sequence of Figure 3 (SEQ ID NO: 13) with glutamine at position 31 designated as the first amino acid (SEQ ID NO: 14). The first 30 amino acids represent a leader sequence not present in the mature protein.

Please replace the paragraph beginning at page 10, line 13 with the following amended paragraph:

Changes in the amino acid sequence at a particular site can be randomly made or specific changes can be selected. Once a specific site is selected it is referred to by its amino acid number designation and by the amino acid found at that site in the wild type SPE-A as shown in Figure 3. The amino acid number designations made in this application are by reference to the sequence in Figure 3 (SEQ ID NO: 13) with the glutamine at position 31 being counted as the first amino acid (SEQ ID NO: 14). Equivalent amino acids corresponding to those identified at a particular site in proteins substantially corresponding to a wild type SPE-A toxin may have different amino acid numbers depending on the reference sequence or if they are fragments. Equivalent residues are also those found in homologous molecules that can be identified as equivalent to amino acids in proteins substantially corresponding to a wild type SPE-A toxin either by comparison of

primary amino acid structure or by comparison to a modeled structure as shown in Figure 1 or by comparison to a known crystal structure of a homologous molecule. It is intended that the invention cover changes to equivalent amino acids at the same or similar locations regardless of their amino acid number designation.